

## SEQUENCE LISTING

&lt;110&gt; Ruben et al.

&lt;120&gt; Human Tumor Necrosis Factor Receptor TR17

&lt;130&gt; PF524P1

&lt;140&gt; Unassigned

&lt;141&gt; 2001-09-25

&lt;150&gt; 60/254,874

&lt;151&gt; 2000-12-13

&lt;150&gt; 60/235,991

&lt;151&gt; 2000-09-26

&lt;150&gt; 09/533,822

&lt;151&gt; 2000-03-24

&lt;150&gt; 60/188,208

&lt;151&gt; 2000-03-10

&lt;160&gt; 7

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 882

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(882)

&lt;400&gt; 1

atg	agt	ggc	ctg	ggc	cgg	agg	cga	ggg	ggc	cgg	agg	cgt	gtg	gac	48
Met	Ser	Gly	Ieu	Gly	Arg	Ser	Arg	Arg	Gly	Gly	Arg	Ser	Arg	Val	Asp
1														15	
5															
10															
15															

cag	gag	gag	cgc	ttt	cca	cag	ggc	ctg	tgg	acg	ggg	gtg	gct	atg	aga	96
Gln	Glu	Glu	Arg	Phe	Pro	Gln	Gly	Ieu	Trp	Thr	Gly	Val	Ala	Met	Arg	
20																
25																
30																

tcc	tgc	ccc	gaa	gag	cag	tac	tgg	gat	cct	ctg	ctg	ggt	acc	tgc	atg	144
Ser	Cys	Pro	Glu	Glu	Gln	Tyr	Trp	Asp	Pro	Leu	Leu	Gly	Thr	Cys	Met	
35																
40																
45																

tcc	tgc	aaa	acc	att	tgc	aac	cat	cag	agg	cag	acc	tgt	gca	gcc	192
Ser	Cys	Lys	Thr	Ile	Cys	Asn	His	Gln	Ser	Gln	Arg	Thr	Cys	Ala	Ala
50															
55															
60															

ttc	tgc	agg	tca	ctc	agc	tgc	cgc	aag	gag	caa	ggc	aag	ttc	tat	gac	240
Phe	Cys	Arg	Ser	Leu	Ser	Cys	Arg	Lys	Glu	Gln	Gly	Lys	Phe	Tyr	Asp	
65																
70																
75																

cat	ctc	ctg	agg	gac	tgc	atc	agc	tgt	gcc	tcc	atc	tgt	gga	cac	288
His	Leu	Leu	Arg	Asp	Cys	Ile	Ser	Cys	Ala	Ser	Ile	Cys	Gly	Gln	His
85															
90															
95															

cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc cca gtg	336
Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val	
100	105
110	
aac ctt cca cca gag ctc agg aga gag cgg agt gga gaa gtt gaa aac	384
Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn	
115	120
125	
aat tca gac aac tcg gga agg tac caa gga ttg gag cac aga ggc tca	432
Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser	
130	135
140	
gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca gat cag gtg	480
Glw Ala Ser Pro Ala Leu Pro Gly Leu Ser Ala Asp Gln Val	
145	150
155	160
gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt gcc gtc ctc tgc	528
Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys	
165	170
175	
tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag agg ggg gat ccc	576
Cys Phe Leu Val Ala Val Ala Cys Leu Lys Lys Arg Gly Asp Pro	
180	185
190	
tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt ccg gcc aag tct	624
Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser	
195	200
205	
tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg agc aca tcc ccc	672
Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro	
210	215
220	
gag cca gtg gag acc tgc agc ttc tgc ttc cct gag tgc agg ggc ccc	720
Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro	
225	230
235	240
240	
acg cag gag agc gca gtc acg cct ggg acc ccc gac ccc act tgt gct	768
Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala	
245	250
255	
gga agg tgg ggg tgc cac acc agg acc aca gtc ctg cag cct tgc cca	816
Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro	
260	265
270	
cac atc cca gac agt ggc ctt ggc att gtg tgt gtg cct gcc cag gag	864
His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu	
275	280
285	
ggg ggc cca ggt gca taa	882
Gly Gly Pro Gly Ala	
290	
<210> 2	
<211> 293	
<212> PRT	
<213> Homo sapiens	
<400> 2	

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp  
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 Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg  
 20 25 30  
 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met  
 35 40 45  
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala  
 50 55 60  
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp  
 65 70 75 80  
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His  
 85 90 95  
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val  
 100 105 110  
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn  
 115 120 125  
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser  
 130 135 140  
 Glu Ala Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val  
 145 150 155 160  
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys  
 165 170 175  
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro  
 180 185 190  
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser  
 195 200 205  
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro  
 210 215 220  
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro  
 225 230 235 240  
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala  
 245 250 255  
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro  
 260 265 270  
 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu  
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 Gly Gly Pro Gly Ala  
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<210> 3  
<211> 733  
<212> DNA  
<213> *Homo sapiens*

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<400> 3
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tctcccgac  tcctggatgg acatgcgtgg tgggtggacgt aacccggaa gaccctgggg 180
tcaagtctaa  ctggtaacgt gacggcggtg aggtgcataa tgccaaagaca aagccgggg 240
aggacgtga  caaacacgcg taccgtgtgg tcacgttcct caccgtctcg caccaggact 300
ggctgtatgg  caaggatgtc aagtgcgtgg tcccaacaaac agccctccca acccccccgg 360
agaaaaacat  ctccaaaaggc aaaggggcgcg cccggaaacc acagggtgtac accctggccc 420
catccccggg  tgatcgacc aagaacccagg tcacgttcgtc ctgcgttggtc aaagggttct 480
atccaaaggc  catcgccgtg gatggggaga gcaatggggca gccggaaaga actaataaga 540
ccacgccttc  ctgtcggtac tccggcggtc ccttttcctt ctcacacaaat ctcacccgtg 600
acaagagcag  gtggcagcag gggaaacgtct ttcgtatgtc cgtgtatgtc gaggtcttcg 660
acaacccata  caccggaaatc agcccttcggcc tggctccgggg taaaatgtatgtc tgacggggcg 720
qactctaaqg  qat

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<210> 4
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)..(5)
<223> Xaa equal any amino acid

<220>
<221> SITE
<222> (9)
<223> Xaa equal any amino acid

<400> 4
Xaa Xaa Xaa Xaa Xaa Glu Gly Ser Xaa
1           5
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<210> 5
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equal is any amino acid

<400> 5
Ala Leu Xaa Asn Asp Glu Gly Ser Gly
1 5

<210> 6
<211> 17
<212> PRT
<213> Homo Sapiens

<400> 6
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Met Leu Gln Asn Ser Ala Val Leu Leu Leu Leu Val Ile Ser Ala Ser  
1 5 10 15

Ala

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<210> 7
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> SIGNAL
<222> (1)..(22)
<223> consensus signal sequence
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Met	Pro	Thr	Trp	Ala	Trp	Trp	Leu	Phe	Leu	Val	Leu	Leu	Leu	Ala	Leu
1					5					10					15
Trp Ala Pro Ala Arg Gly															
20															